



SEQUENCE LISTING

<110> Schulein, Martin
Bjornvad, Mads

<120> Family 9 Endo-Beta-1, 4-Glucanases

<130> 5843.200-US

<160> 10

<170> PatentIn version 3.1

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<211> 1941

<212> DNA

<213> Bacillus licheniformis

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Ala Ser Phe Ser Glu Lys Thr Arg Ala Ala Ser Ala Glu Glu Tyr Pro

-10 -5 -1 1

cat aat tat gct gaa ctg ctg caa aag tct ttg tta ttt tat gaa gca 144
His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala

5 10 15

cag cgc tcg gga aga ctt ccg gaa aac agc cgg ctg aat tgg aga gga 192
Gln Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly

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gac tcc ggg ctt gag gac gga aaa gac gtt ggc ctc gat tta acg gga 240
Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly

40 45 50

ggg tgg tat gat gcc ggc gac cac gtg aag ttc ggt ctg ccg atg gct 288
Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala

55 60 65

RECEIVED
FEB 12 2003
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tac aaa gaa tcg ggt cag ctt gat gcg gcg ctg gac aat att aaa tgg Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp 85 90 95	384
gcg aca gac tac ttt ctt aaa gcc cat acg gct cct tat gaa ttg tgg Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp 100 105 110 115	432
ggc caa gtc gga aat ggc gct cta gac cac gca tgg tgg ggg ccg gcc Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala 120 125 130	480
gaa gta atg ccg atg aag cgc cct gcc tat aag atc gat gcc ggc tgt Glu Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys 135 140 145	528
ccg ggg tca gac ctt gct ggt ggt aca gcc gca gcg cta gca tca gca Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala 150 155 160	576
tca att att ttc aag ccg aca gat tct tct tac tct gaa aaa tta ctg Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu 165 170 175	624
gct cat gcc aag caa ttg tat gat ttt gcc gac cgc tac cgc ggc aaa Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys 180 185 190 195	672
tat tca gac tgc att aca gac gca cag caa tat tat aat tcg tgg agc Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser 200 205 210	720
ggg tat aaa gat gaa ctg aca tgg gga gct gtc tgg ctc tac ttg gca Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala 215 220 225	768
aca gaa gaa caa caa tat ttg gat aaa gcc ctt gct tcg gtc tca gat Thr Glu Glu Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp 230 235 240	816
tgg ggc gat ccc gca aac tgg cct tac cgc tgg acg ctt tcc tgg gat Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp 245 250 255	864
gac gtc act tac gga gca cag ctg ctg ctc gct cgt ctg aca aac gat Asp Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp 260 265 270 275	912
tcc cgt ttt gtc aaa tct gtc gaa cgc aat ctt gat tat tgg tcg aca Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr 280 285 290	960

ggc tac agt cat aat gga agc ata gaa cgg atc acg tat acg ccg ggc Gly Tyr Ser His Asn Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly 295 300 305	1008
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cag atg aat gtg cct gaa aac cat cgc cat acc cta tac ggc gca tta Gln Met Asn Val Pro Glu Asn His Arg His Thr Leu Tyr Gly Ala Leu 390 395 400	1296
gtc ggc ggt ccg gga agg gac gat tcg tac cga gat gac ata aca gat Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp 405 410 415	1344
tat gcg tca aac gaa gtt gcg atc gat tat aat gcc gct ttt acc ggc Tyr Ala Ser Asn Glu Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly 420 425 430 435	1392
aac gta gcg aaa atg ttt cag ctg ttc ggg aaa ggc cat gtt ccg ctg Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu 440 445 450	1440
cct gat ttt ccg gag aag gaa aca cct gag gac gaa tat ttt gca gag Pro Asp Phe Pro Glu Lys Glu Thr Pro Glu Asp Glu Tyr Phe Ala Glu 455 460 465	1488
gca tca atc aac agc tcc gga aac agc tat act gaa atc cgg gcg cag Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Glu Ile Arg Ala Gln 470 475 480	1536
ctc aat aac cgt tcg gga tgg ccg gca aag aaa acc gat caa ttg tct Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Gln Leu Ser 485 490 495	1584
ttc cgc tac tac gtt gac ttg acg gaa gct gta gaa gcg gga tat tcc Phe Arg Tyr Tyr Val Asp Leu Thr Glu Ala Val Glu Ala Gly Tyr Ser 500 505 510 515	1632
gcc gaa gat ata aaa gtc aca gcc ggc tat aac gaa ggg gcc tcg gta	1680

Ala Glu Asp Ile Lys Val Thr Ala Gly Tyr Asn Glu Gly Ala Ser Val	
520 525 530	
tca gag ctg aag ccg cat gac gct tca aag cac att tac tat aca gaa	1728
Ser Glu Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Glu	
535 540 545	
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Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His	
550 555 560	
aaa aaa gaa gtg cag ttc cgc ctt tcg gca cca gac gga acg tct ttt	1824
Lys Lys Glu Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe	
565 570 575	
tgg aac ccg gaa aat gac cac tct tat cag ggt ctg tca cat gcg ctt	1872
Trp Asn Pro Glu Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu	
580 585 590 595	
ctg aag acg cgg tat att cct gtt tat gat gat gga cgg ctc gtt ttc	1920
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-10 -5 -1 1

His Asn Tyr Ala Glu Leu Leu Gln Lys Ser Leu Leu Phe Tyr Glu Ala
5 10 15

Gln Arg Ser Gly Arg Leu Pro Glu Asn Ser Arg Leu Asn Trp Arg Gly
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Asp Ser Gly Leu Glu Asp Gly Lys Asp Val Gly Leu Asp Leu Thr Gly
40 45 50

Gly Trp Tyr Asp Ala Gly Asp His Val Lys Phe Gly Leu Pro Met Ala
55 60 65

Tyr Ser Ala Ala Ile Leu Ser Trp Ser Val Tyr Glu Tyr Arg Asp Ala
70 75 80

Tyr Lys Glu Ser Gly Gln Leu Asp Ala Ala Leu Asp Asn Ile Lys Trp
85 90 95

Ala Thr Asp Tyr Phe Leu Lys Ala His Thr Ala Pro Tyr Glu Leu Trp
100 105 110 115

Gly Gln Val Gly Asn Gly Ala Leu Asp His Ala Trp Trp Gly Pro Ala
120 125 130

Glu Val Met Pro Met Lys Arg Pro Ala Tyr Lys Ile Asp Ala Gly Cys
135 140 145

Pro Gly Ser Asp Leu Ala Gly Gly Thr Ala Ala Ala Leu Ala Ser Ala
150 155 160

Ser Ile Ile Phe Lys Pro Thr Asp Ser Ser Tyr Ser Glu Lys Leu Leu
165 170 175

Ala His Ala Lys Gln Leu Tyr Asp Phe Ala Asp Arg Tyr Arg Gly Lys
180 185 190 195

Tyr Ser Asp Cys Ile Thr Asp Ala Gln Gln Tyr Tyr Asn Ser Trp Ser
200 205 210

Gly Tyr Lys Asp Glu Leu Thr Trp Gly Ala Val Trp Leu Tyr Leu Ala
215 220 225

Thr Glu Glu Gln Gln Tyr Leu Asp Lys Ala Leu Ala Ser Val Ser Asp
230 235 240

Trp Gly Asp Pro Ala Asn Trp Pro Tyr Arg Trp Thr Leu Ser Trp Asp
245 250 255

Asp Val Thr Tyr Gly Ala Gln Leu Leu Leu Ala Arg Leu Thr Asn Asp
260 265 270 275

Ser Arg Phe Val Lys Ser Val Glu Arg Asn Leu Asp Tyr Trp Ser Thr
280 285 290

Gly Tyr Ser His Asn Gly Ser Ile Glu Arg Ile Thr Tyr Thr Pro Gly
295 300 305

Gly Leu Ala Trp Leu Glu Gln Trp Gly Ser Leu Arg Tyr Ala Ser Asn
310 315 320

Ala Ala Phe Leu Ala Phe Val Tyr Ser Asp Trp Val Asp Thr Glu Lys
325 330 335

Ala Lys Arg Tyr Arg Asp Phe Ala Val Arg Gln Thr Glu Tyr Met Leu
340 345 350 355

Gly Asp Asn Pro Gln Gln Arg Ser Phe Val Val Gly Tyr Gly Lys Asn
360 365 370

Pro Pro Lys His Pro His His Arg Thr Ala His Gly Ser Trp Ala Asn
375 380 385

Gln Met Asn Val Pro Glu Asn His Arg His Thr Leu Tyr Gly Ala Leu
390 395 400

Val Gly Gly Pro Gly Arg Asp Asp Ser Tyr Arg Asp Asp Ile Thr Asp
405 410 415

Tyr Ala Ser Asn Glu Val Ala Ile Asp Tyr Asn Ala Ala Phe Thr Gly
420 425 430 435

Asn Val Ala Lys Met Phe Gln Leu Phe Gly Lys Gly His Val Pro Leu
440 445 450

Pro Asp Phe Pro Glu Lys Glu Thr Pro Glu Asp Glu Tyr Phe Ala Glu
455 460 465

Ala Ser Ile Asn Ser Ser Gly Asn Ser Tyr Thr Glu Ile Arg Ala Gln
470 475 480

Leu Asn Asn Arg Ser Gly Trp Pro Ala Lys Lys Thr Asp Gln Leu Ser
485 490 495

Phe Arg Tyr Tyr Val Asp Leu Thr Glu Ala Val Glu Ala Gly Tyr Ser
500 505 510 515

Ala Glu Asp Ile Lys Val Thr Ala Gly Tyr Asn Glu Gly Ala Ser Val
520 525 530

Ser Glu Leu Lys Pro His Asp Ala Ser Lys His Ile Tyr Tyr Thr Glu
535 540 545

Val Ser Phe Ser Gly Val Leu Ile Tyr Pro Gly Gly Gln Ser Ala His
550 555 560

Lys Lys Glu Val Gln Phe Arg Leu Ser Ala Pro Asp Gly Thr Ser Phe
565 570 575

Trp Asn Pro Glu Asn Asp His Ser Tyr Gln Gly Leu Ser His Ala Leu
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Gly His Glu Pro Gly Tyr
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